

FIGURE 1

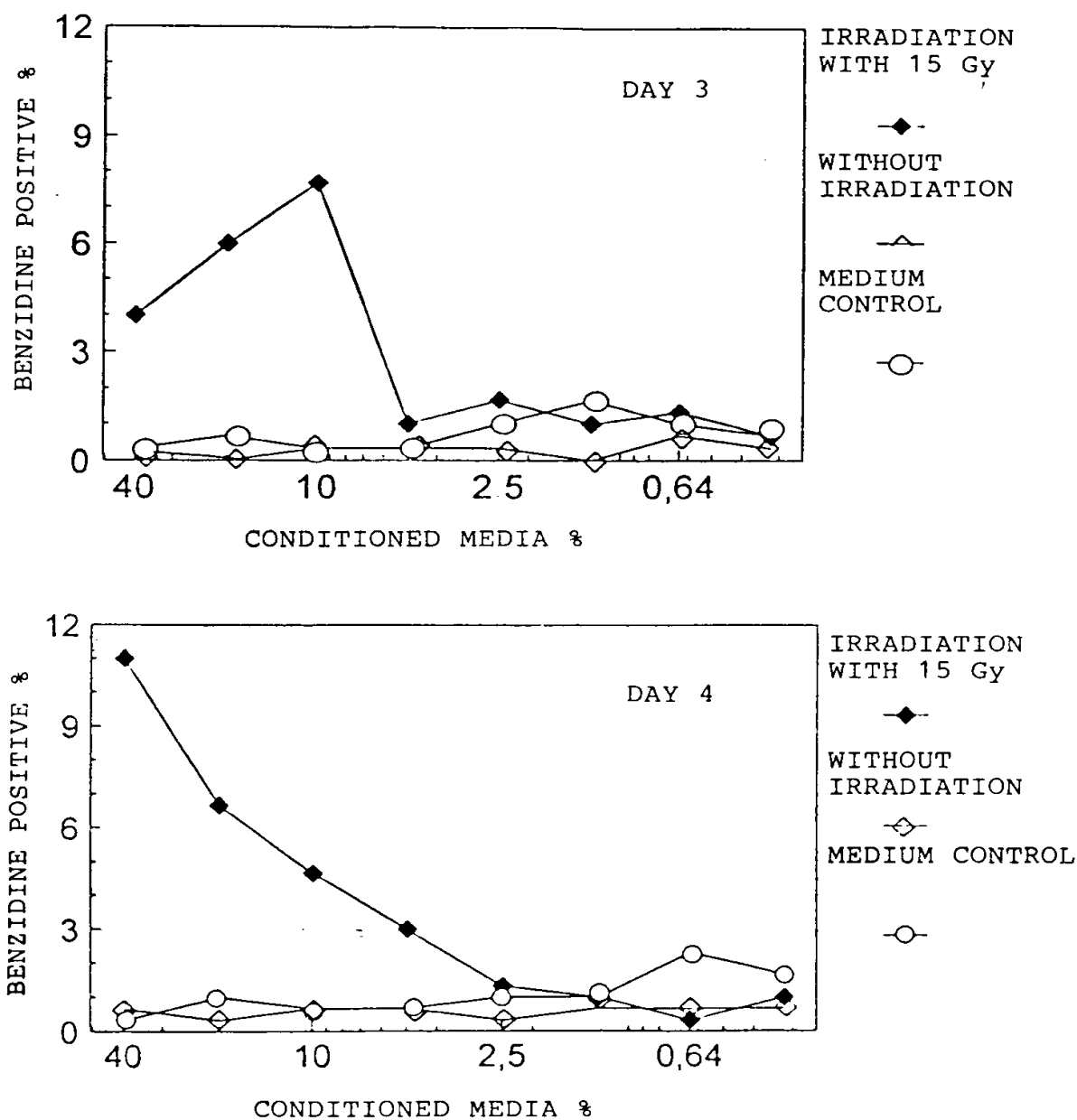


FIGURE 2

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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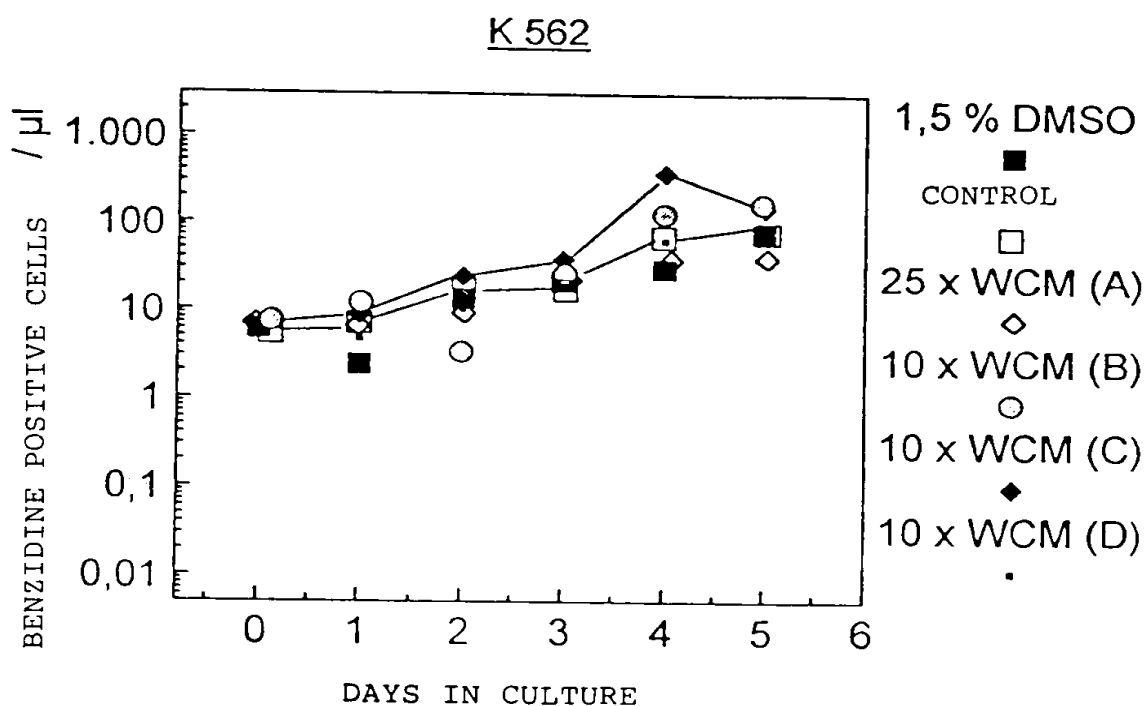


FIGURE 3

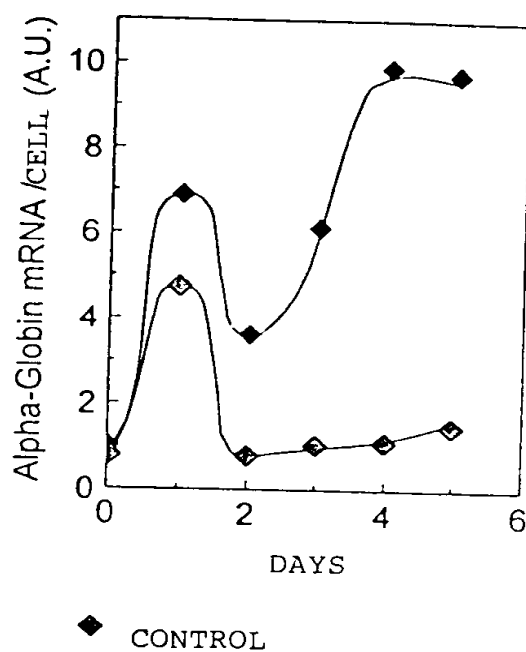
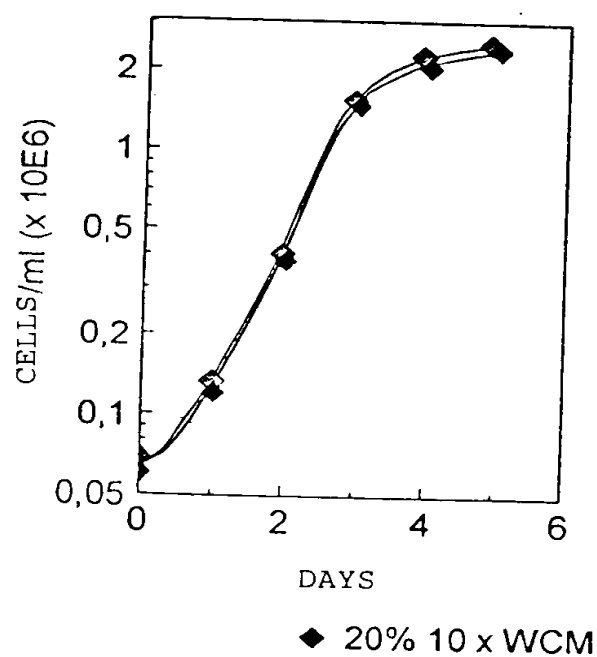


FIGURE 4

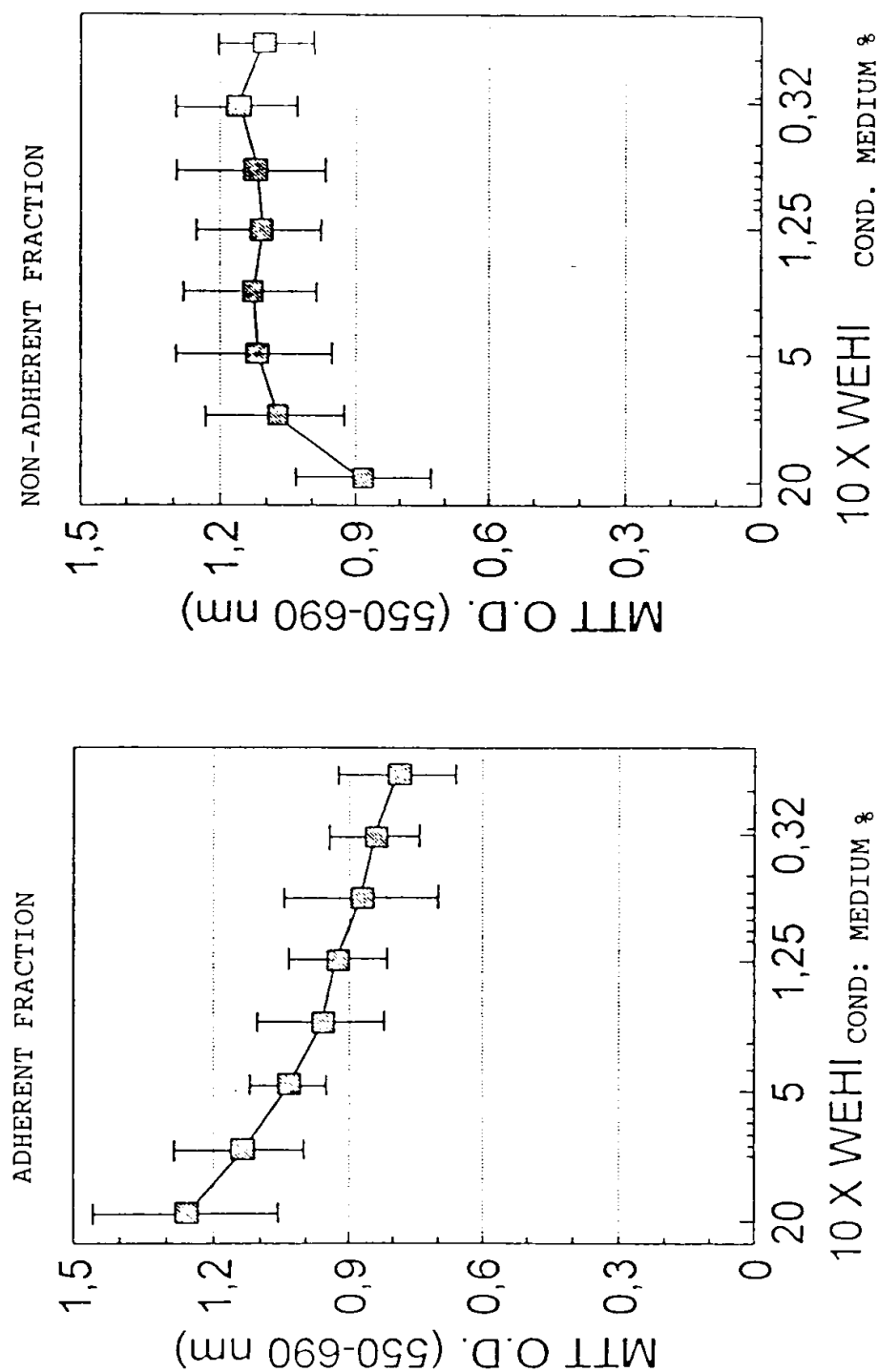


FIGURE 5

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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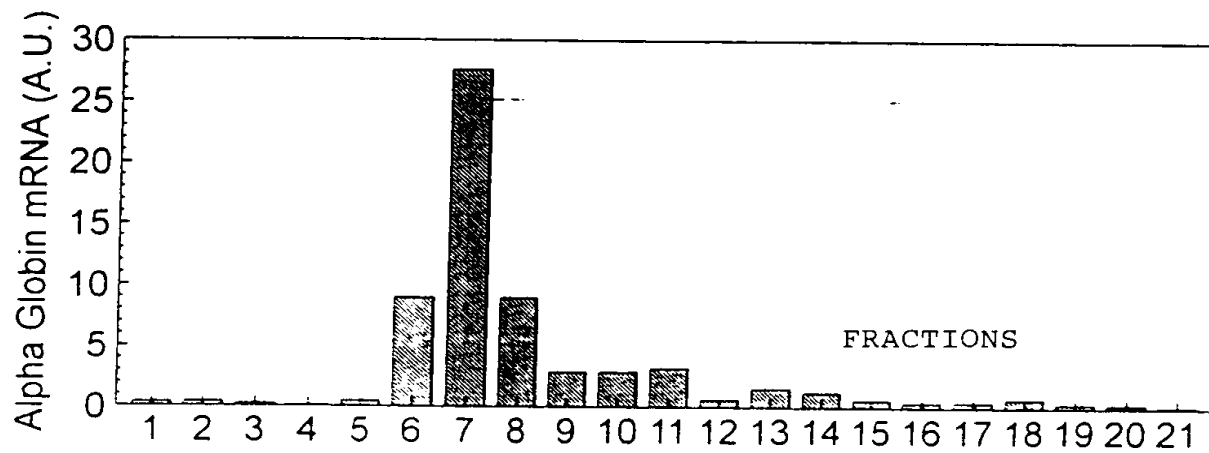


FIGURE 6

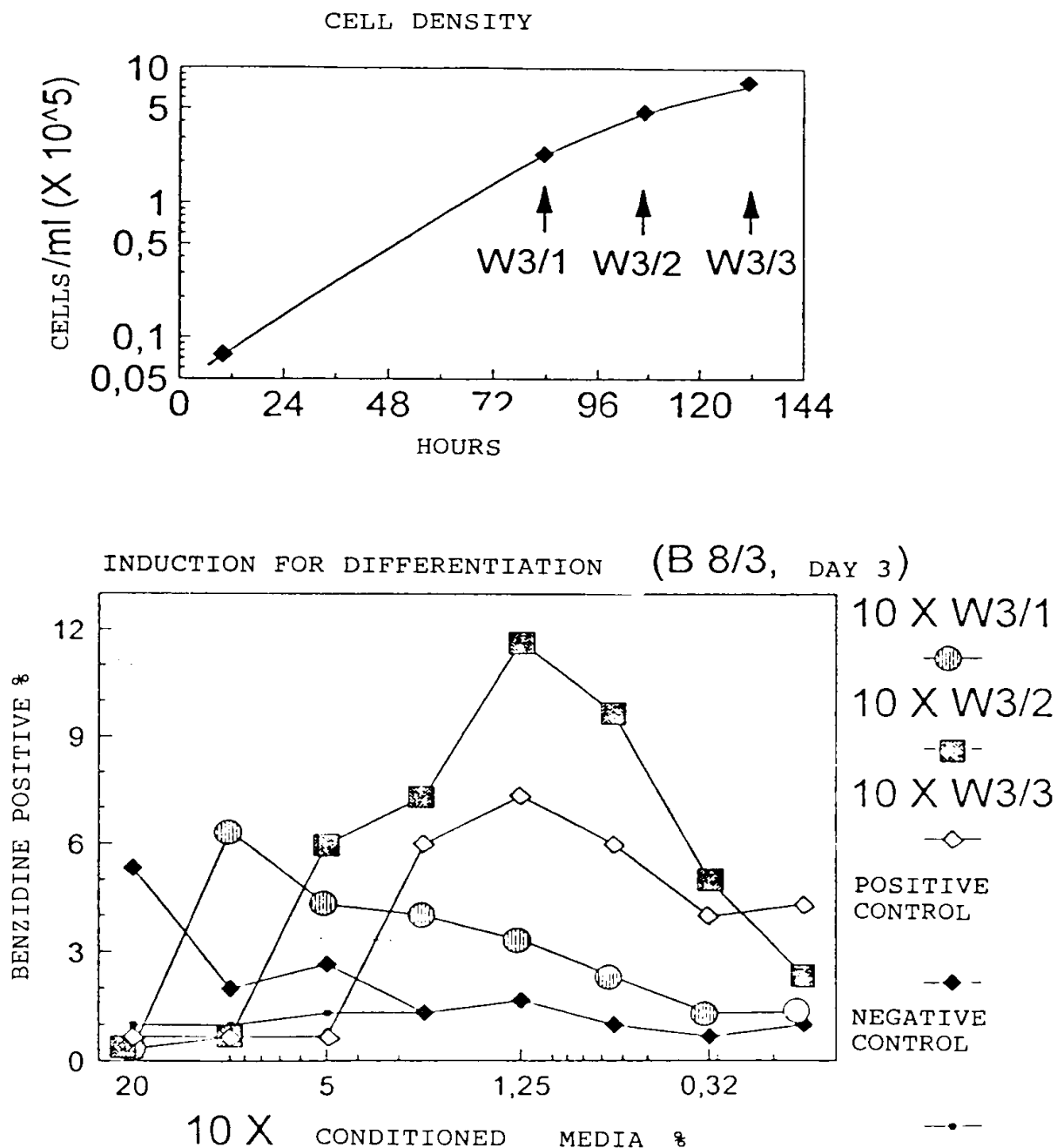


FIGURE 7

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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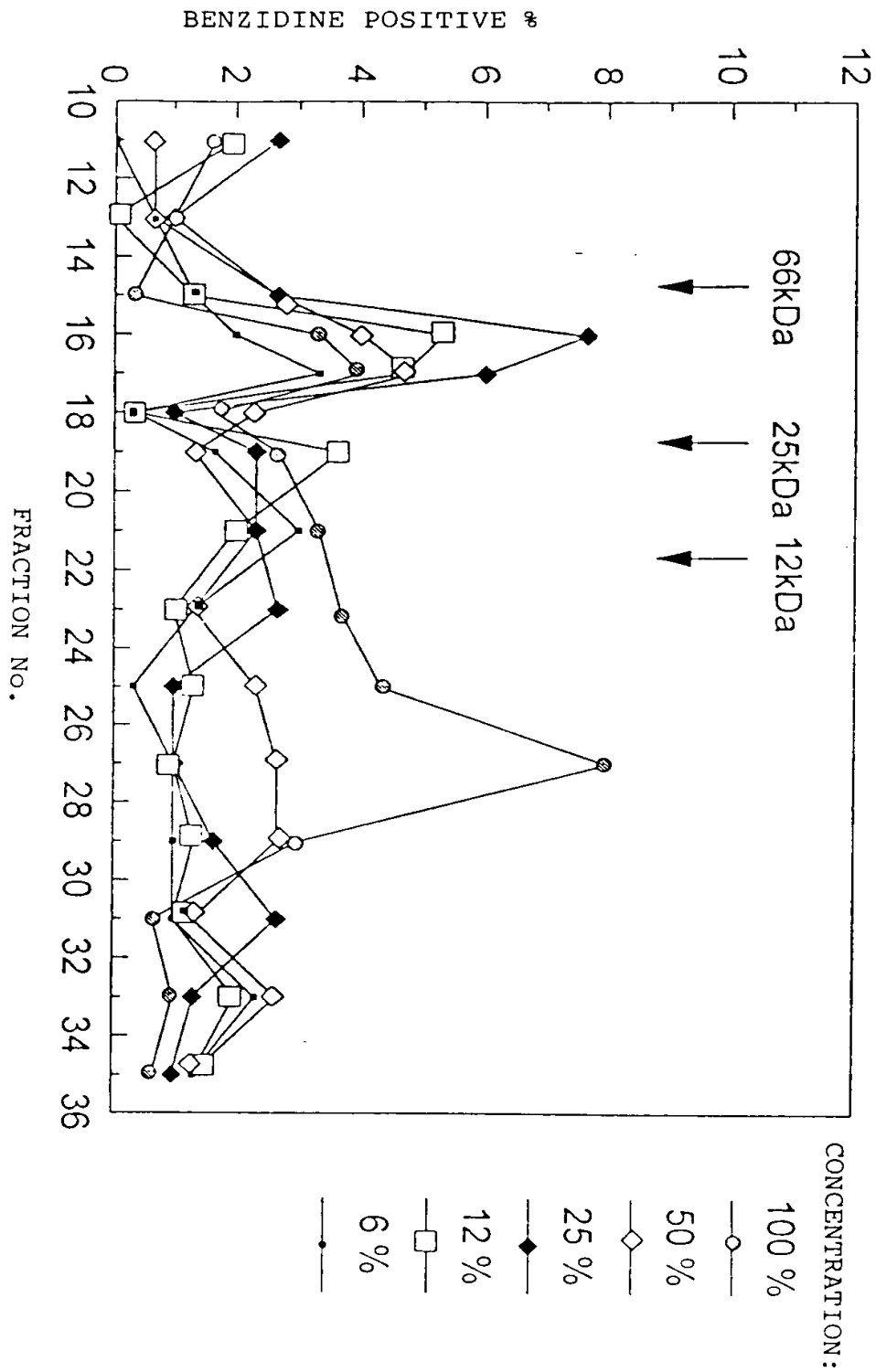


FIGURE 8

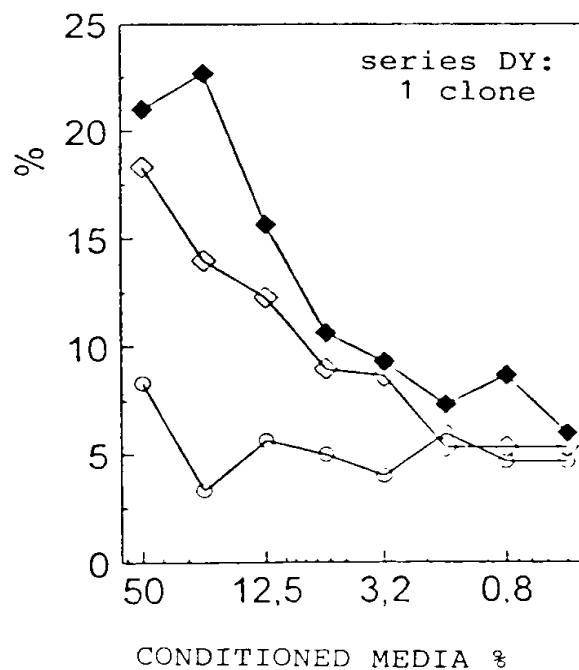
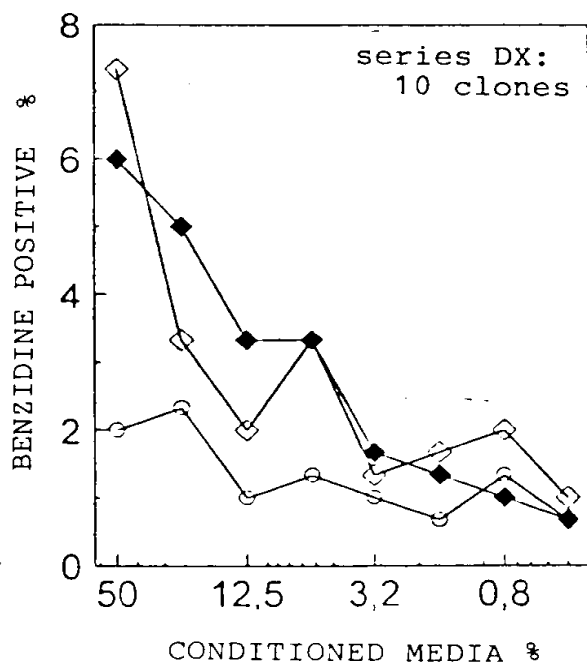
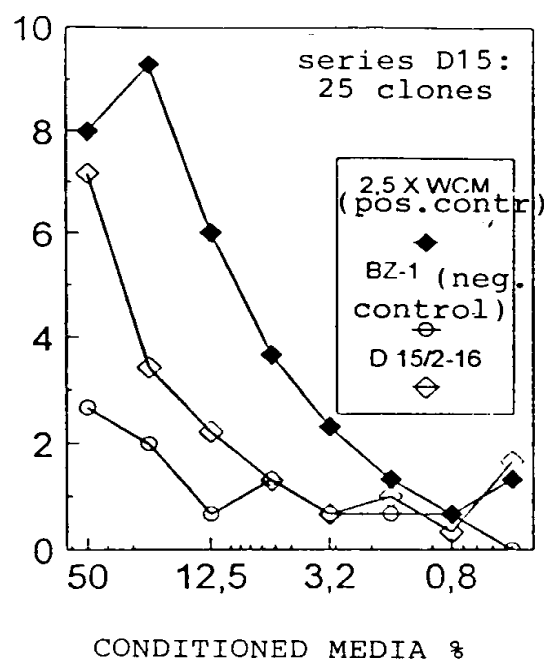
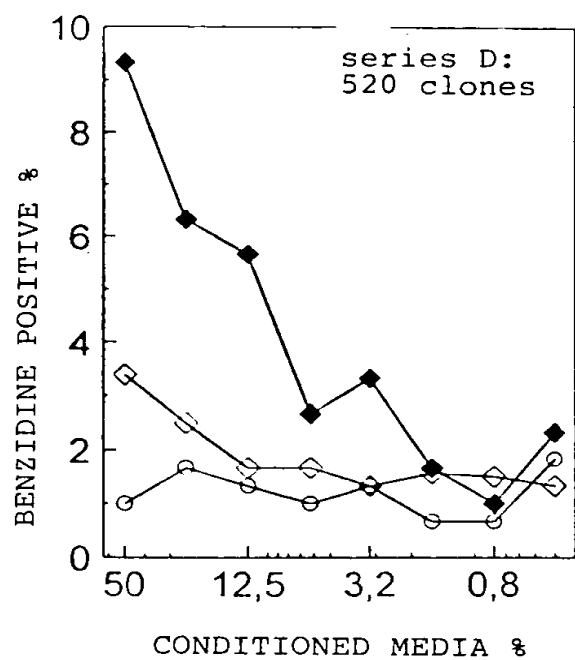


FIGURE 9

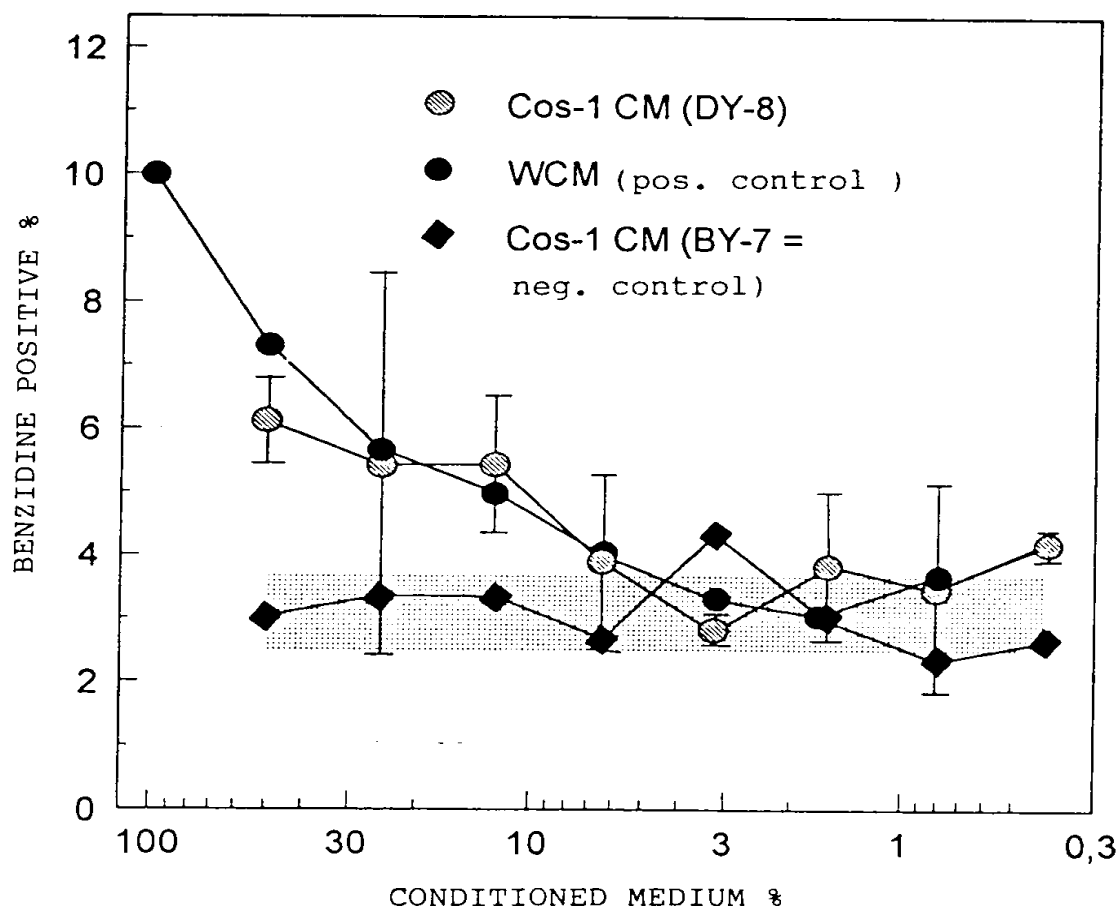


FIGURE 10

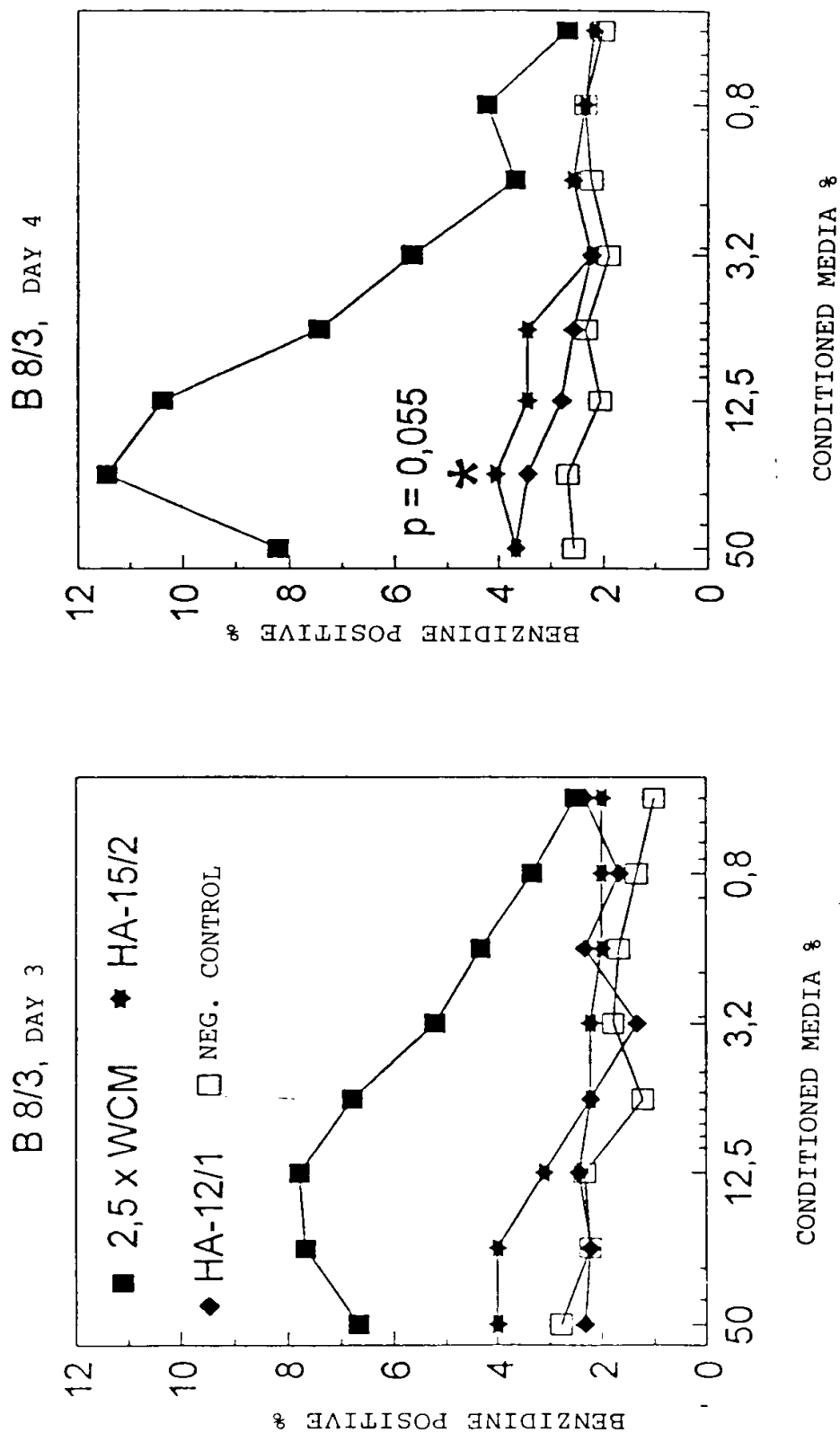


FIGURE 11

APPROVED	O.G. FIG.	
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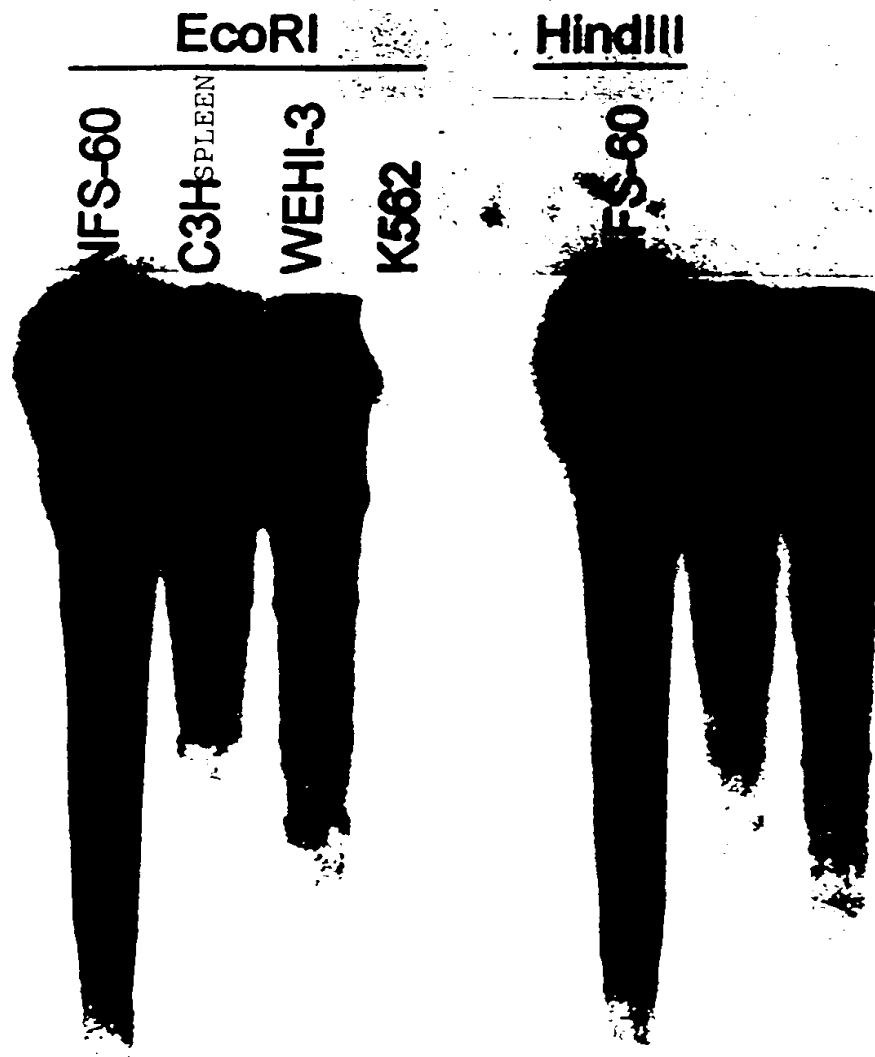


FIGURE 12

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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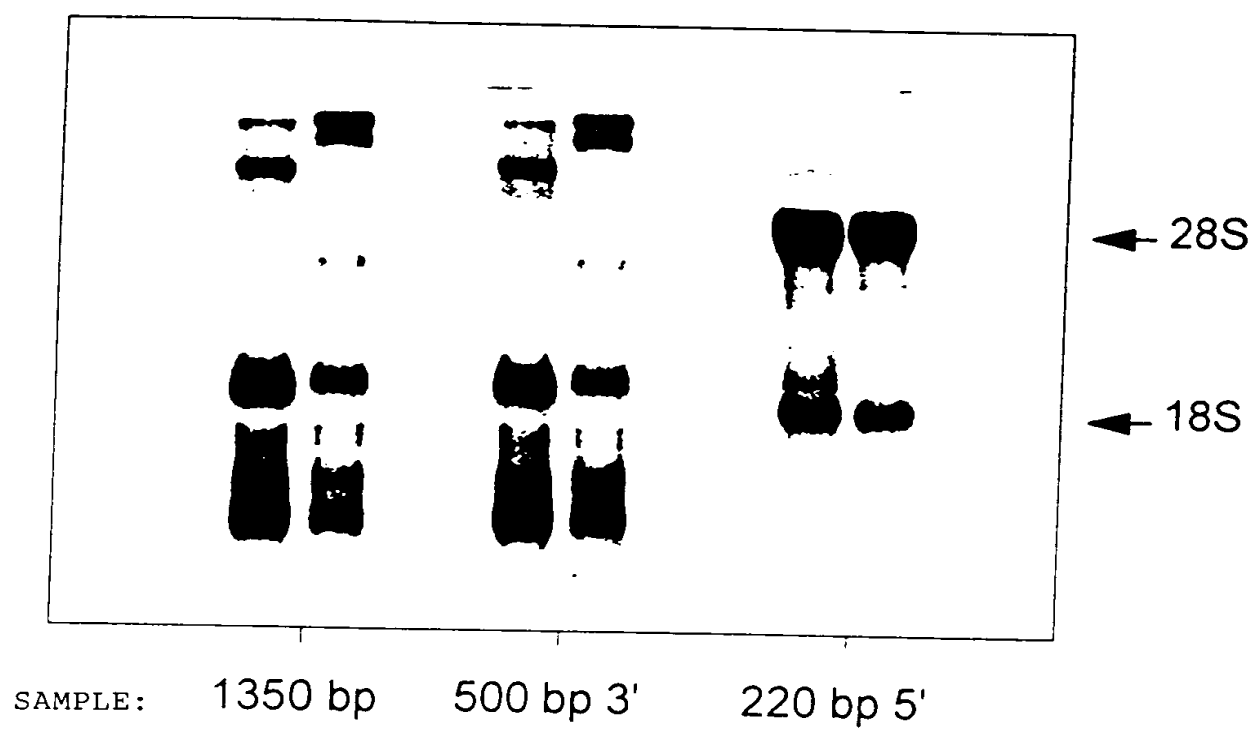


FIGURE 13

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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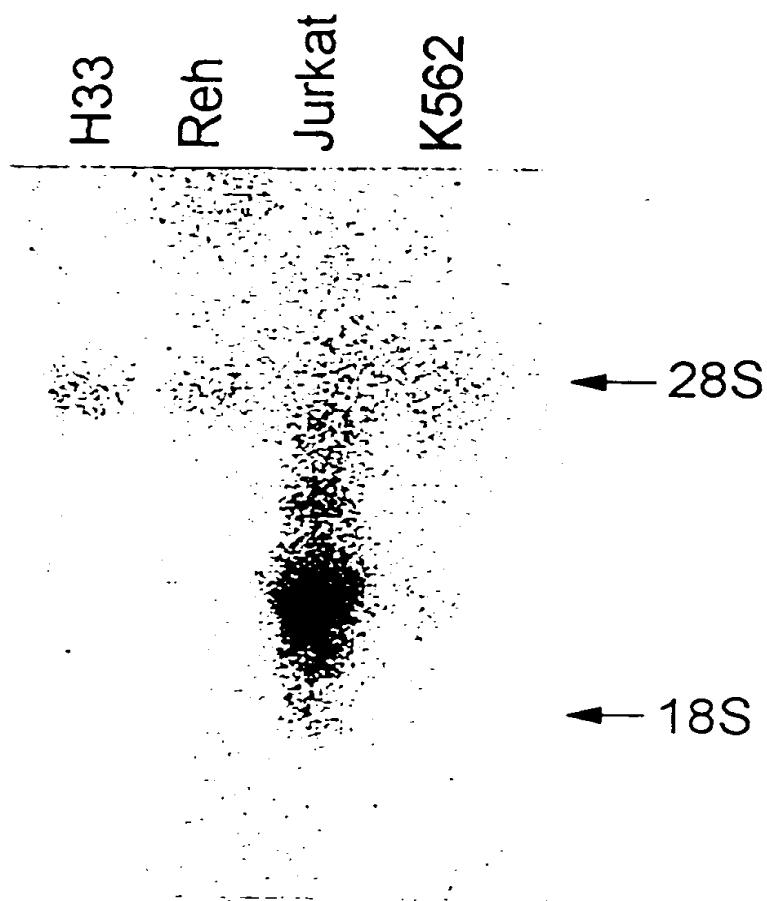
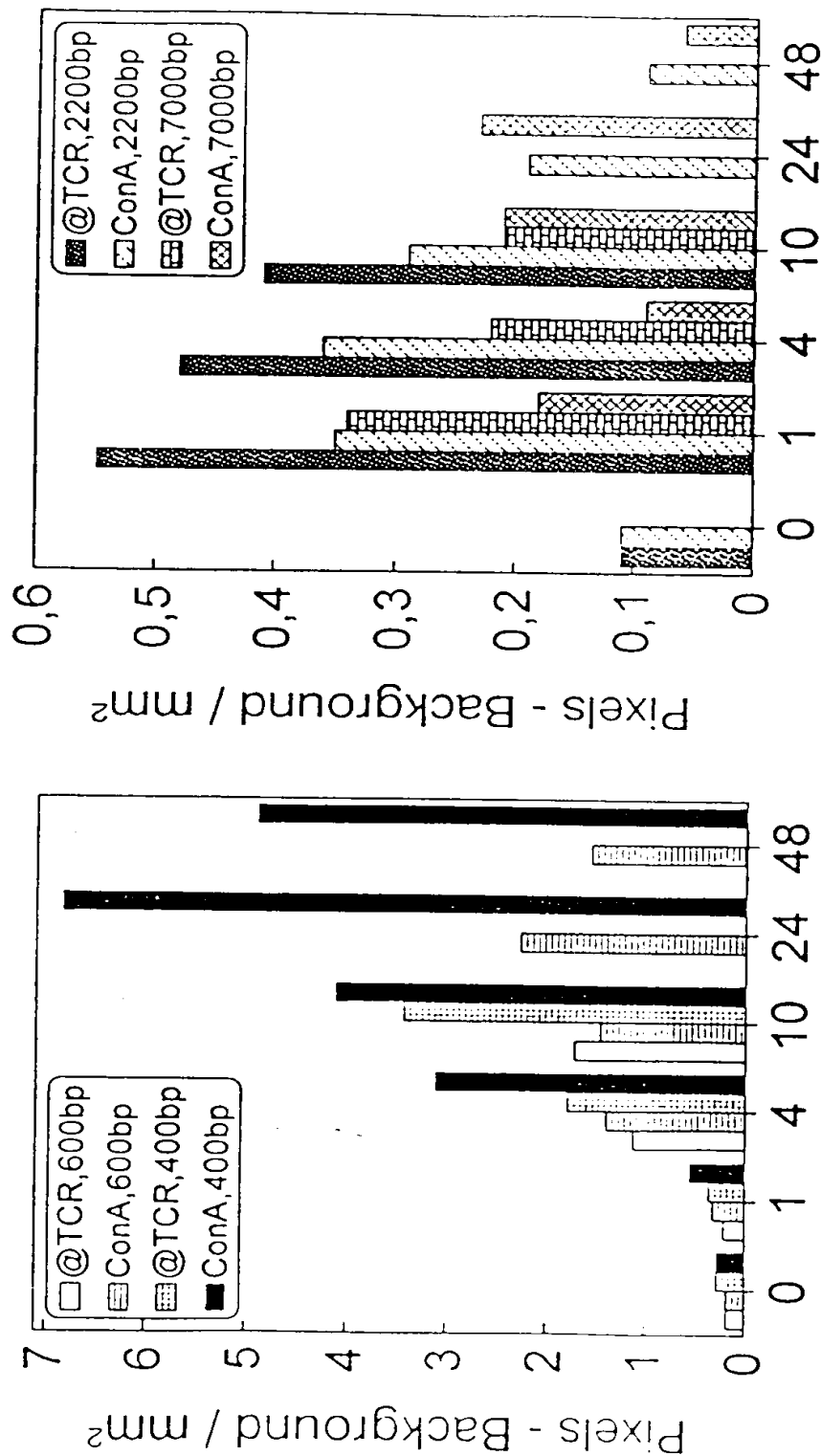


FIGURE 14



HOURS IN CULTURE

FIGURE 15

APPROVED	O.G. FIG.	
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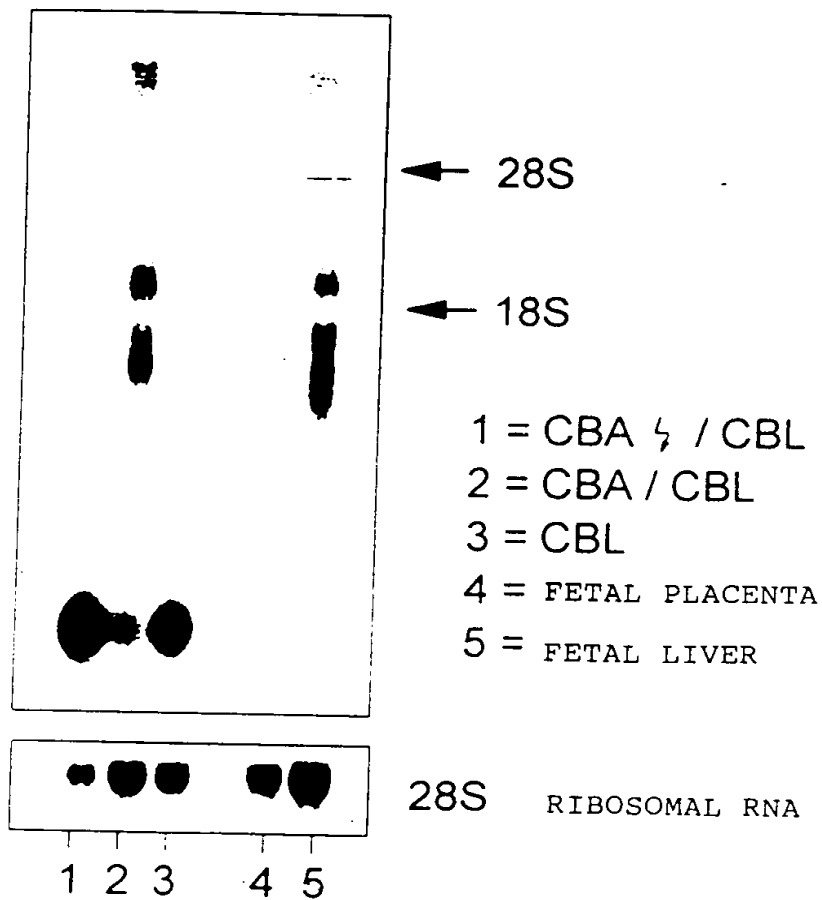


FIGURE 16

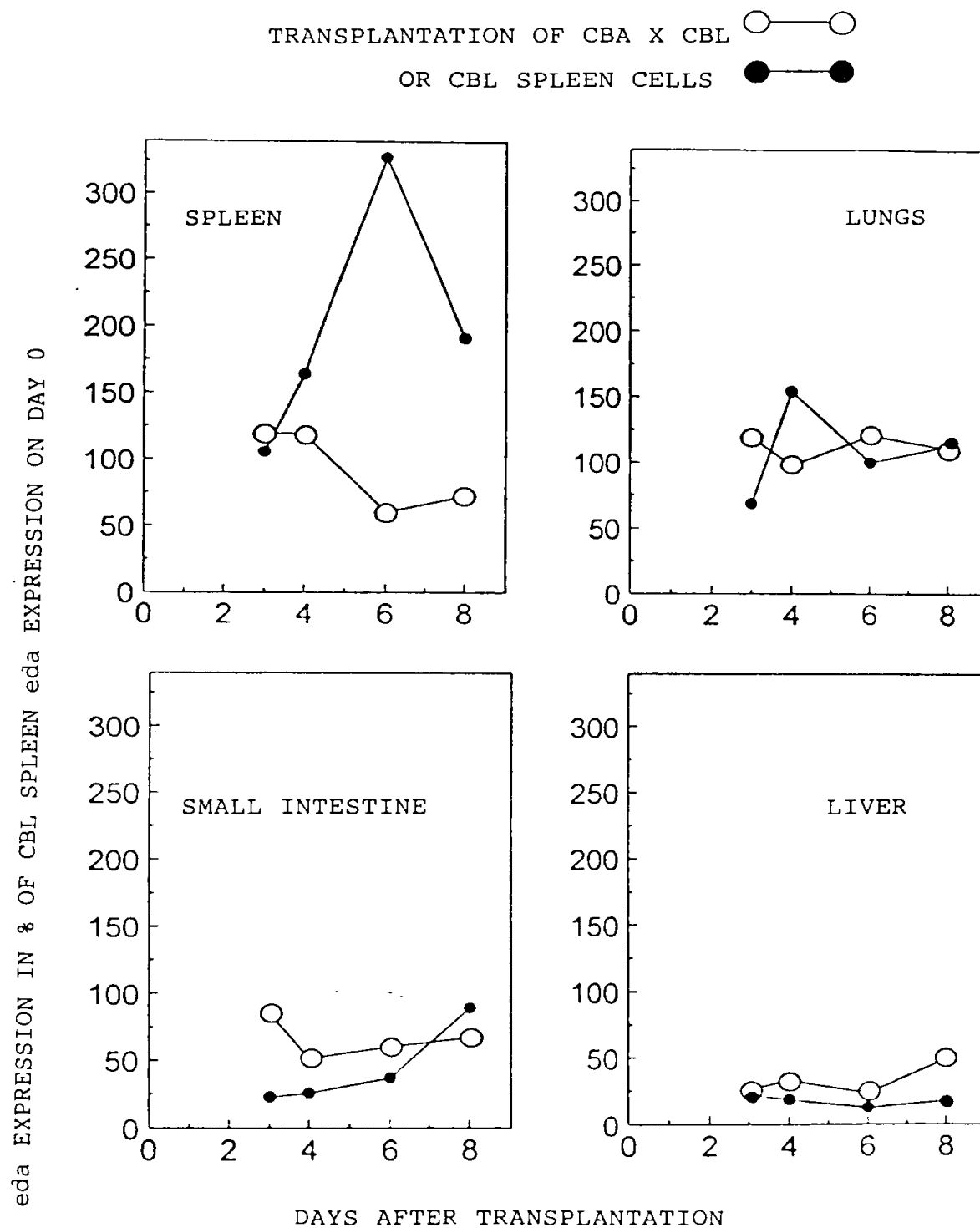


FIGURE 17

APPROVED	O.G. FIG.	
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1  CCGACCGTGC GGAAGCTCGG TCGGAGCCGG GAATGCTGGG ACTTGTAGTG CGTAGTCAAT
51 GAAGGCTCGG TCGGAGCCGG GAATGCTGGG ACTTGTAGTG CGTAGTCAAT
101 GGTTCTCTAT GGGCTTTCAG AGTGAGTGGC GGGAAGGCGG CCCCAGGGCA
151 TGCTGGGAGT TGTAATCCTG CCGTCGTCAA TGGTTCTCTA TGGGCTTTC
201 GAGTGAGTGG CGGGAAGGCG GCGGAGGAGG ATGCTGGGAG TTGTAGTCCT
251 GCCATAGTCA ATGGTCTCTT ATGGGCTTTC AGACTGAGTG GCGGGAAGGC
301 GCGGAGGAGG CATGCTGGGA GTTGCAGCGC CATGTTTTAA AGCACGCGTT
351 TCTCTGTATA GACCTGGCTG TGGATTTTTC GCTAATTCTT TTTTCTAGCT
401 TTATTTTAA TTTTACTTT TTCACACAGG ATTTCTCTTT ATAGCCTTGG
451 CTACCGTTTT TTCCCTAATT ATTCTCCTTT TCATTTTGGT TTATTTTCTT
501 TTAATTTTGG TTTTCTAAG ACAGGGTTTC TCTGTATAGA CCTGGCTGTG
551 GATTTCTCAC TAATTATTTT TTTTAGCTTT ATTTTAAATT TTTACTTTTT
601 CACACAGGAT TTCTCTTTAT AGCCTTGGCT ACCGTTTTTT CCGTAATTAT
651 TCTTATTTTC ATTTTGGTTT ATTTTCTAAT TTTAATTTT GATTTTGGAG
701 ACAGGGTTTC TCTTTTAGCC GCAGCTATGG TTTCTGCCCT AATTATTCTT
751 GTCCTTATTT GTAATTTAAT TCTTAATTTA ATTTAATTTA TAATTTTGT
801 GTAAGTTTTT CTGTGGGCGT GAATGGAAAG TCTAACCCGT GTTCTCTGT
851 TCAGCGTCCG CCGGTCACGG CCGCCGCCCC CAGCGACGTC ACCCACACGC
901 GCAGAAGCGG ACGCCGCGGT CAAGATGTCT CTGCCATGCC CACGGGACGC
951 ACGGACGCAC GGACGGACGG ACGGACTCCA CAAGGTAGGA AGCCTGCGCC
1001 GACCGCACCG CCGCACCCAC CACAGCACAC AGGACACACG CCGGCCCCCG
1051 GCGCGCCAG GCACACGCGG CACACACGGC ACACACGGCA GGCAGGCCAG
1101 GCACACGCAT CCGCAGGACC CGCCGCACCC GCCACGCAGA CACGGACGAG
1151 CCGCCGCGGT CAAGATGTTC ACCCGCCGCG GTCAAGATGT ATGTGCCACC
1201 GACCTCTGCC CCGCTGGACG GACGGACGGA CGCACGCACG CCGTCAGCGT
1251 CCACCGGTCA CTGCCGCCGC CCACAGTGAT GTCACCCACG AAAGCACACA
1301 CGTAGAAGCG GACGCCGTGG TCAAGATGTC TCTGCCATCC CCACAGGACG
1351 GACGGACGGA CTCCACAAGG TGCGCGTGTC GCCGAGGCCG CCAGGACGGA
1401 GCGATTCTCA CGGAGGAAGG AGCACGCCAA CAGGGCCTGA CTGCGTACAG
1451 ACATGTCCCC CTCAATAAAA TTGCAGTTGA AATGGAAAAA AAAAA

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FIGURE 18

APPROVED	O.G. FIG.	
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PRELIMINARY STRUCTURE OF eda 2.2 kbp cDNA

* = stopcodon, R = Repeat

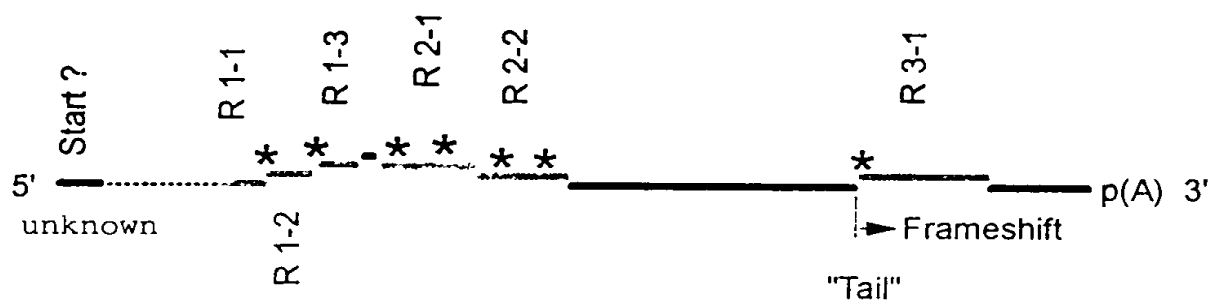


FIGURE 19

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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1  CGCGCCCGCC CGGGATCCCC AGCTGCCGCC GCGCCCGCCC GCCCGCCCGG
                                CONSENSUS SEQUENCE
51  GGGCCCGCT GCAGAACCGT GACCGTCCGC CGGTCACGGC CGCCGCCCCC
    ATGGGGCT GCAGAACCGT GACCGTCCGC CGGTCACGGC CGCCGCCCCC
101 AGCGACGTCA CCCACACGCG CAGAAGCGGA CGCCGCGGTC AAGATGTCTC
    AGCGACGTCA CCCACACGCG CAGAAGCGGA CGCCGCGGTC AAGATGTCTC
151 TGCCATGCCC ACGGGACGCA CGGACGCACG GACGGACGGA CTGACTCCAC
    TGCCATGCCC ACGGGACGCA CGGACGCACG GACGGACGGA CTGACTCCAC
201 AAGGTAGGAA GCCTGCGCCG ACCGCACCGC CGCACCCACC ACAGCACACA
    AAGGTAGGAA GCCTGCGCCG ACCGCACCGC CGCACCCACC ACAGCACACA
251 GGACACACGC GGGCCCCGCG CCCGCCCAGG CACACGCGGC ACACACGGCA
    GGACACACGC GGGCCCCGCG CCCGCCCAGG CACACGCGGC ACACACGGCA
301 CACACGGCAG GCAGGCCAGG CACACGCATC CGCAGGACCC GCCGCACCCG
    CACACGGCAG GCAGGCCAGG CACACGCATC CGCAGGACCC GCCGCACCCG
351 CCACGCAGAC ACGGACGAGC CGCCGCGGTC AAGATGTTCA CCCGCCGCGG
    CCACGCAGAC ACGGACGAGC CGCCGCGGTC AAGATGTTCA CCCGCCGCGG
401 TCAAGATGTA TGTGCCACCG ACCCTCGCCC CGCTGGACGG ACGGACGGAC
    TCAAGATGTA TGTGCCACCG ACCCTCGCCC CGCTGGACGG ACGGACGGAC
451 GCGCGCACGC CGTCAGCGTC CACCGGTCAC TGCCGCCGCC CACAGTGACG
    GCGCGCACGC CGTCAGCGTC CACCGGTCAC TGCCGCCGCC CACAGTGACG
501 TCACCCACGA AAGCACACAC GTAGAAGCGG ACGCCGTGGT CAAGATGTCT
    TCACCCACGA AAGCACACAC GTAGAAGCGG ACGCCGTGGT CAAGATGTCT
551 CTGCCATCCC CACAGGACGG ACGGACGGAC TCCACAAGGT GCGCGTGTCTG
    CTGCCATCCC CACAGGACGG ACGGACGGAC TCCACAAGGT GCGCGTGTCTG
601 CCGAGGCCGC CAGGATGGAG CGATTCTCAC GGAGGAAGGA GCACGCCAAC
    CCGAGGCCGC CAGGATGGAG CGATTCTCAC GGAGGAAGGA GCACGCCAAC
651 AGGGCCTGAC TGCGTACAGA AATGCCCCC CTCAATAAAA TTGCAGTTGA
    AGGGCCTGAC TGCGTACAGA AATGCCCCC CTCAATAA
701 AATGGAAAAA AAAAA

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FIGURE 20

APPROVED	O.G. FIG.	
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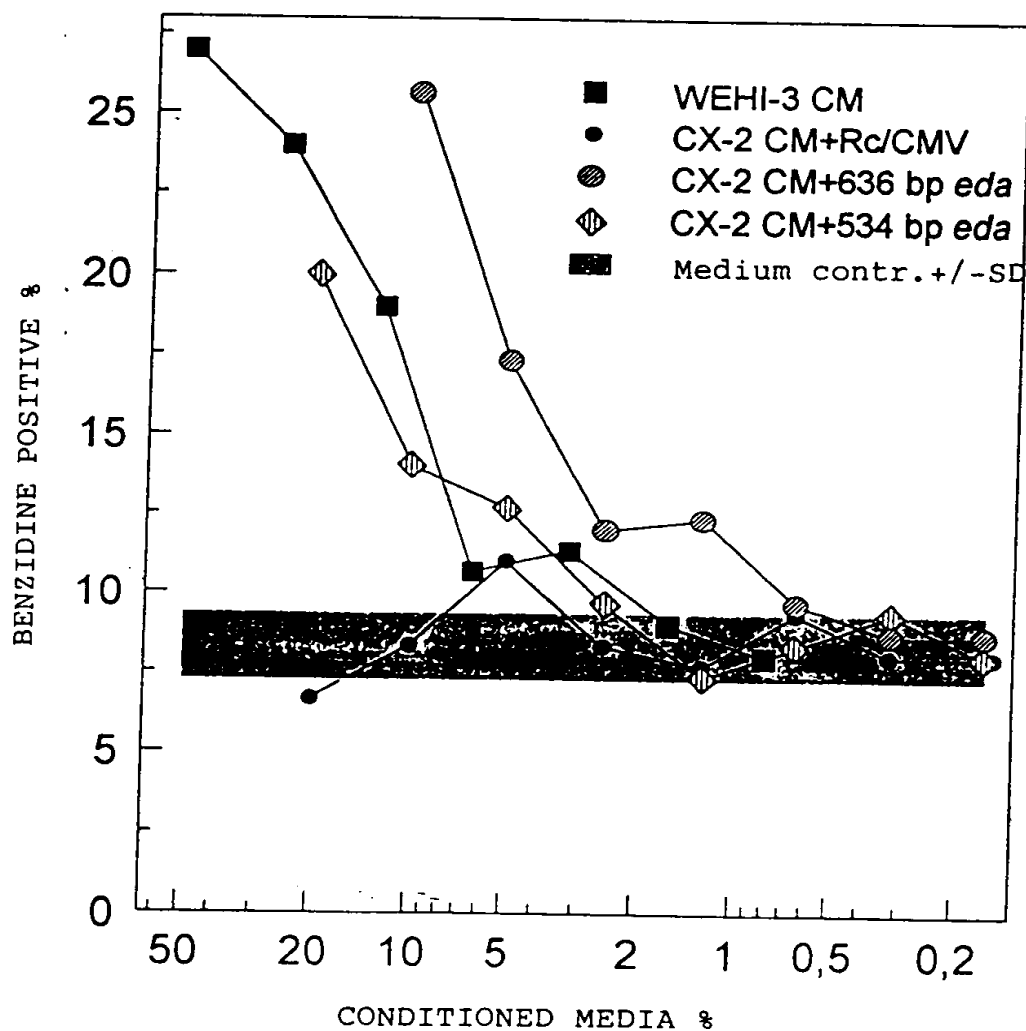
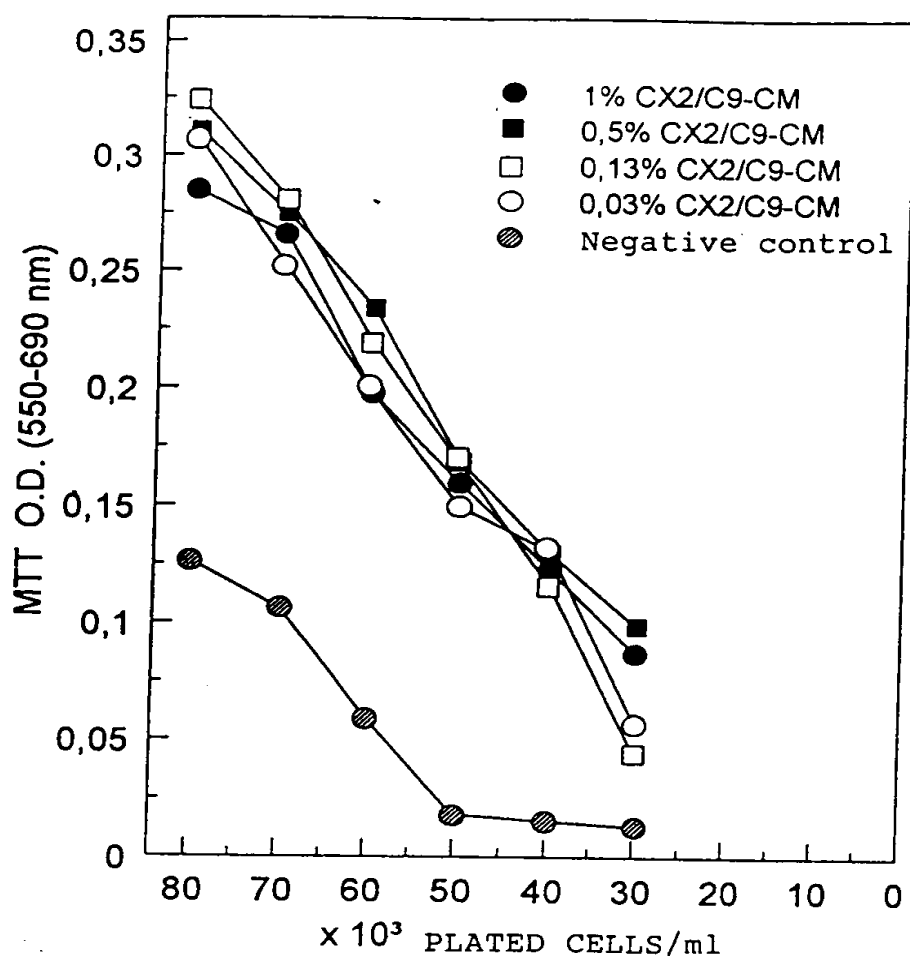


FIGURE 21

A



B

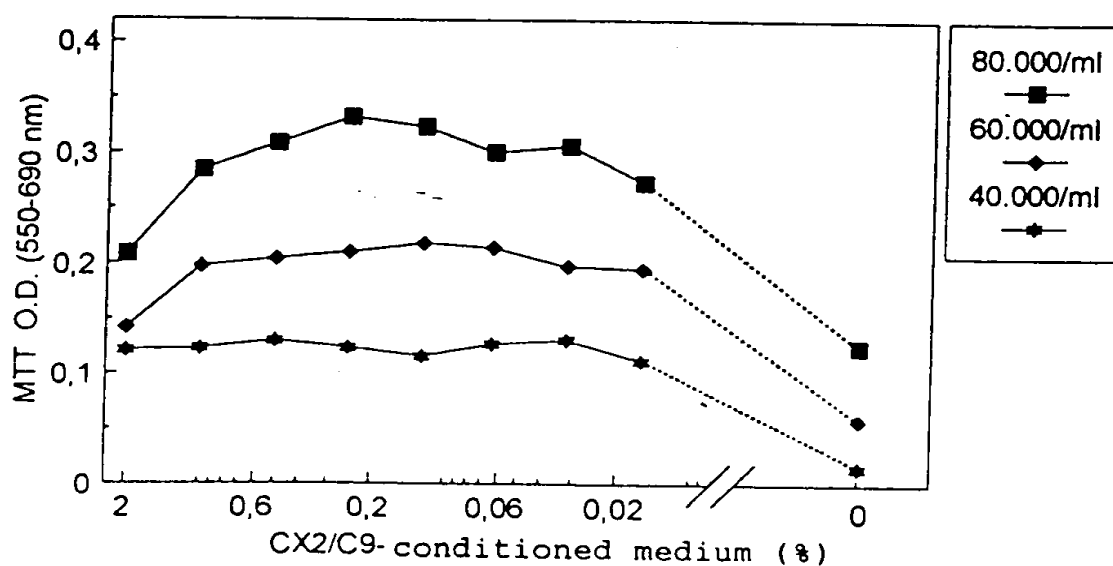


FIGURE 22

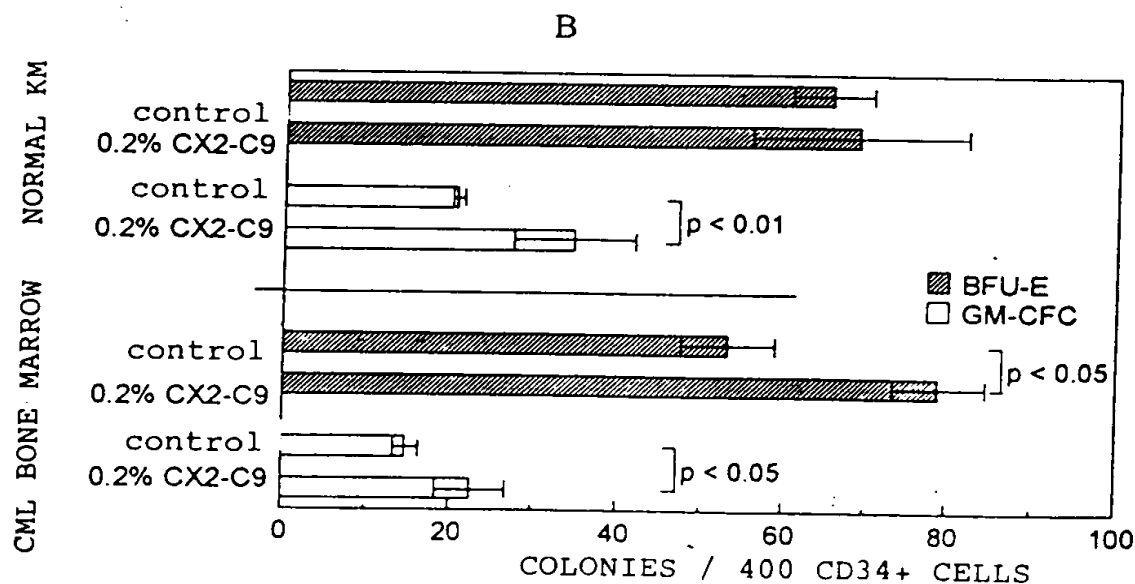
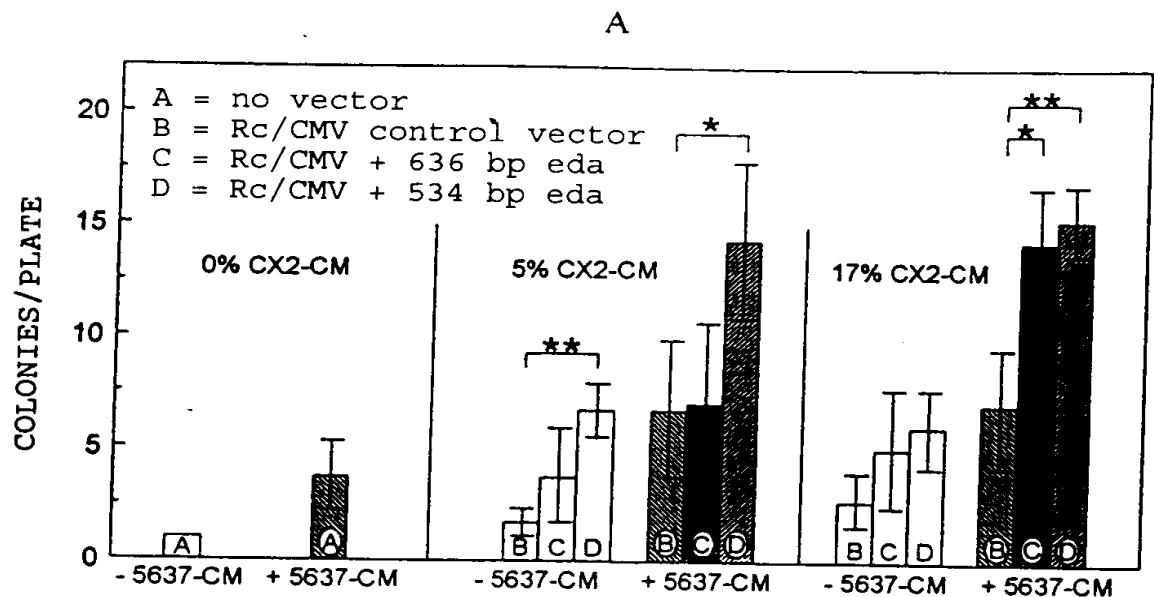


FIGURE 23